GENOME RESEARCH
Volume 21 Issue 12 December 2011

Research

(continued)

Methods

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(continued)

[OA]Open Access paper.

Cover Human reference genomes, represented by circles; the arcs inside each circle symbolize highly related sequenced genomes (i.e., individuals from the same family or population). The colorful abstract segments on each arc show common and rare structural variation events among individual genomes. The CommonLAW package presented in this issue introduces novel combinatorial formulations and algorithms for structural variation discovery among a number of sequenced donor genomes, with the help of a complete reference genome. CommonLAW significantly reduces the false positive rate in detecting structural variation events when compared with conventional methods. (Cover illustration by Azalia Musa, modified by Andres Wanner [http://www.pixelstorm.ch/] and Iman Hajirasouliha, Simon Fraser University. For details, see Hormozdiari et al., pp. 2203–2212.])